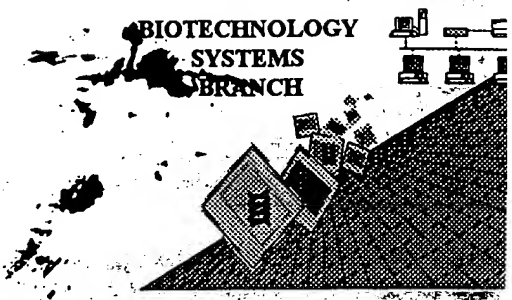
Pasted

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/367,013

Art Unit / Team No. : 1652

Date Processed by STIC: 5/5/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/367,013*

INPUT SET: S35428.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed
errors throughout

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
--> **(B) ~~(B)~~ FILING DATE:**
delete (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: WARD, MICHAEL R.
(B) REGISTRATION NUMBER: 38,651
(C) REFERENCE/DOCKET NUMBER: CGAB-210

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A

46

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
--> **(A) LENGTH: 227 amino acids** 228 shown
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
1               5                  10                  15
His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
            20                  25                  30
Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
            35                  40                  45
Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
            50                  55                  60
Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
            65                  70                  75
Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
            80                  85                  90
Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
            95                  100                 105
Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
            110                 115                 120
Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
            125                 130                 135
Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
            140                 145                 150
Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
            155                 160                 165
Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
            170                 175                 180
Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
            185                 190                 195
Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
            200                 205                 210
Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
            215                 220                 225
Asp Asp Xaa
```

---

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids 102 shown
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Phe Trp Lys Xaa Pro Ser Xaa Pro Arg Xaa Xaa Gln Val Xaa Gly
1               5                  10                  15
Ala Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
            20                  25                  30
Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
        35                  40                  45
Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
    50                  55                  60
Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
65                  70                  75
Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
65 80               70 85               75 90
Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
80                  85
95                  100
```

---

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 520 nucleic acids ← This should be
(B) TYPE: amino acid nucleic acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Boxes below are in bold print due to above error.

```
GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG    60
CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC   120
ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG   180
GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT   240
GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCCA   300
CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC   360
ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC   420
TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC   480
```

```
--dC 980  TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTCCCGC                  520
     981
     982

     1043  (2) INFORMATION FOR SEQ ID NO:26:
     1044
     1045       (i) SEQUENCE CHARACTERISTICS:
-->  1046            (A) LENGTH: 125 amino acids
     1047            (B) TYPE: amino acid
     1048            (C) STRANDEDNESS: Not Relevant
     1049            (D) TOPOLOGY: linear
     1050
     1051       (ii) MOLECULE TYPE: peptide
     1052
     1053       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
     1054
     1055
     1056  Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
     1057  1               5                  10                  15
     1058  Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
     1059                  20                  25                  30
     1060  Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
     1061                  35                  40                  45
     1062  Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
     1063                  50                  55                  60
     1064  Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
     1065                  65                  70                  75
     1066  Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
     1067                  80                  85                  90
     1068  Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
     1069                  95                  100                 105
     1070  His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
     1071                  110                 115                 120
     1072  Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
     1073                  125
     1074  Arg Lys Val Arg Pro
     1075
     1076

     1478  (2) INFORMATION FOR SEQ ID NO:34:
     1479
     1480       (i) SEQUENCE CHARACTERISTICS:
-->  1481            (A) LENGTH: 411 amino acids
     1482            (B) TYPE: amino acid
     1483            (C) STRANDEDNESS: single
     1484            (D) TOPOLOGY: linear
     1485
     1486       (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)
     1487
     1488       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
     1489
     1490
     1491  His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
```

```
1492  1               5                   10                  15
1493  Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
1494                  20                  25                  30
1495  Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
1496                  35                  40                  45
1497  Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
1498                  50                  55                  60
1499  Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
1500                  65                  70                  75
1501  Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
1502                  80                  85                  90
1503  Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
1504                  95                  100                 105
1505  Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
1506                 110                 115                 120
1507  Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
1508                 125                 130                 135
1509  Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
1510                 140                 145                 150
1511  Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
1512                 155                 160                 165
1513  Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile
1514                 170                 175                 180
1515  Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
1516                 185                 190                 195
1517  Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
1518                 200                 205                 210
1519  Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
1520                 215                 220                 225
1521  Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
1522                 230                 235                 240
1523  His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
1524                 245                 250                 255
1525  Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
1526                 260                 265                 270
1527  His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
1528                 275                 280                 285
1529  Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
1530                 290                 295                 300
1531  Glu Met Val Leu Glu Xaa Ile Ser Leu Val Pro Lys Gly Phe Phe
1532                 305                 310                 315
1533  Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr Xaa Thr
1534                 320                 325                 330
1535  Xaa Asp Gln Xaa Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
1536                 335                 340                 345
1537  Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe Xaa Thr Val
1538                 350                 355                 360
1539  Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu Xaa
1540                 365                 370                 375
1541  Leu Val Tyr Tyr Arg His Xaa Gly Cys Phe Thr His Val Cys His
1542                 380                 385                 390
1543  Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
1544                 400                 405                 410
```

395 400 405

1545 Arg
1546

1593 (2) INFORMATION FOR SEQ ID NO:36:
1594
1595 (i) SEQUENCE CHARACTERISTICS:
--> 1596 **(A) LENGTH: 86 amino acids** 87 shown
1597 (B) TYPE: amino acid
1598 (C) STRANDEDNESS: single
1599 (D) TOPOLOGY: linear
1600
1601 (ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)
1602
1603 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
1604
1605
1606

```
1607 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
1608 1               5                  10                  15
1609 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
1610             20                  25                  30
1611 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
1612             35                  40                  45
1613 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
1614             50                  55                  60
1615 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
1616             65                  70                  75
1617 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa
1618             80                  85
```

1619
1620
1621

1679 (2) INFORMATION FOR SEQ ID NO:38:
1680
1681 (i) SEQUENCE CHARACTERISTICS:
--> 1682 **(A) LENGTH: 566 amino acids** 562
1683 (B) TYPE: amino acid
1684 (C) STRANDEDNESS: single
1685 (D) TOPOLOGY: linear
1686
1687 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)
1688
1689 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1690
1691

```
1692 His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe
1693 1               5                  10                  15
1694 Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val
1695             20                  25                  30
1696 Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu
1697             35                  40                  45
1698 Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His
```

```
1699                    50                  55                  60
1700  Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
1701                    65                  70                  75
1702  Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp
1703                    80                  85                  90
1704  Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile
1705                    95                  100                 105
1706  Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu
1707                    110                 115                 120
1708  Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr
1709                    125                 130                 135
1710  Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg
1711                    140                 145                 150
1712  Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
1713                    155                 160                 165
1714  Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile
1715                    170                 175                 180
1716  Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys
1717                    185                 190                 195
1718  Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu
1719                    200                 205                 210
1720  Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
1721                    215                 220                 225
1722  Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
1723                    230                 235                 240
1724  Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg
1725                    245                 250                 255
1726  Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val
1727                    260                 265                 270
1728  Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp
1729                    275                 280                 285
1730  Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His
1731                    290                 295                 300
1732  Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
1733                    305                 310                 315
1734  Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly
1735                    320                 325                 330
1736  Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser
1737                    335                 340                 345
1738  Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala
1739                    350                 355                 360
1740  Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala
1741                    365                 370                 375
1742  Leu Val Leu Gln Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser
1743                    380                 385                 390
1744  Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu His Ser Pro Xaa
1745                    400 395             405 400             410 405
1746  Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu
1747                    415                 420                 425
1748  Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly
1749                    430                 435                 440
1750  Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
1751                    445                 450                 455
```

```
1752  Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
1753                  460                 465                 470
1754  Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
1755                  475                 480                 485
1756  Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
1757                  490                 495                 500
1758  Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
1759                  505                 510                 515
1760  Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
1761                  520                 525                 530
1762  Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
1763                  535                 540                 545
1764  Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
1765                  550                 555                 560
1766  Pro Gly Asp Val Gly Pro Xaa
1767                  565
1768
1769
```

```
1770  (2) INFORMATION FOR SEQ ID NO:39:
1771
1772       (i) SEQUENCE CHARACTERISTICS:
-->1773            (A) LENGTH: 619 amino acids
1774               (B) TYPE: amino acid
1775               (C) STRANDEDNESS: single
1776               (D) TOPOLOGY: linear
1777
1778       (ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)
1779
1780       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1781
1782
1783
1784  Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
1785  1                   5                  10                  15
1786  Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
1787                   20                  25                  30
1788  Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
1789                   35                  40                  45
1790  Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
1791                   50                  55                  60
1792  Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
1793                   65                  70                  75
1794  Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val
1795                   80                  85                  90
1796  Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys
1797                   95                 100                 105
1798  Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly
1799                  110                 115                 120
1800  Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met
1801                  125                 130                 135
1802  Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
1803                  140                 145                 150
```

```
1804  Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
1805                  155                 160                 165
1806  Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu
1807                  170                 175                 180
1808  Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met
1809                  185                 190                 195
1810  Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu
1811                  200                 205                 210
1812  Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe
1813                  215                 220                 225
1814  Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
1815                  230                 235                 240
1816  Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser
1817                  245                 250                 255
1818  Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu
1819                  260                 265                 270
1820  Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys
1821                  275                 280                 285
1822  Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg
1823                  290                 295                 300
1824  Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn
1825                  305                 310                 315
1826  Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu Val Tyr Ala
1827                  320                 325                 330
1828  Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe Leu Leu Ser
1829                  335                 340                 345
1830  Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser Trp Asp
1831                  350                 355                 360
1832  Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro Val
1833                  365                 370                 375
1834  Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly
1835                  380                 385                 390
1836  Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly
1837                  400 395             405 400             410 405
1838  Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala
1839                  415                 420                 425
1840  Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu
1841                  430                 435                 440
1842  Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu
1843                  445                 450                 455
1844  Pro Ala Trp Leu His Ser Pro Xaa Arg Leu Pro Leu Val His Pro
1845                  460                 465                 470
1846  Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
1847                  475                 480                 485
1848  Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly
1849                  490                 495                 500
1850  Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
1851                  505                 510                 515
1852  Ser Pro Pro Pro His His Xaa Ser Ala Leu Thr Leu Gly Phe His
1853                  520                 525                 530
1854  Gly Pro His Ser Thr Ala Ser Pro Thr Xaa Ala Cys Asp Leu Gly
1855                  535                 540                 545
1856  Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa Leu Ser Arg Gly Ser
```

numbering off by 5

```
1857                    550                 555                 560
1858  Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
1859                    565                 570                 575
1860  Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
1861                    580                 585                 590
1862  Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
1863                    595                 600                 605
1864  Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xaa
1865                    610                 615                 620
1866
1867
1868
```

```
1869  (2) INFORMATION FOR SEQ ID NO:40:
1870
1871       (i) SEQUENCE CHARACTERISTICS:
-->1872         (A) LENGTH: 757 amino acids
1873            (B) TYPE: amino acid
1874            (C) STRANDEDNESS: single
1875            (D) TOPOLOGY: linear
1876
1877       (ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)
1878
1879       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
1880
1881
1882  Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
1883  1                5                  10                  15
1884  Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
1885                   20                  25                  30
1886  Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
1887                   35                  40                  45
1888  Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
1889                   50                  55                  60
1890  Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
1891                   65                  70                  75
1892  Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
1893                   80                  85                  90
1894  Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
1895                   95                 100                 105
1896  Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
1897                  110                 115                 120
1898  Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
1899                  125                 130                 135
1900  Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
1901                  140                 145                 150
1902  Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp
1903                  155                 160                 165
1904  Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
1905                  170                 175                 180
1906  Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly
1907                  185                 190                 195
1908  Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala
```

```
1909                    200                 205                 210
1910  Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His
1911                    215                 220                 225
1912  Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys
1913                    230                 235                 240
1914  Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe
1915                    245                 250                 255
1916  Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln
1917                    260                 265                 270
1918  Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala
1919                    275                 280                 285
1920  Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro
1921                    290                 295                 300
1922  Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg
1923                    305                 310                 315
1924  Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His
1925                    320                 325                 330
1926  Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser
1927                    335                 340                 345
1928  Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn
1929                    350                 355                 360
1930  Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu
1931                    365                 370                 375
1932  Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu
1933                    380                 385                 390
1934  Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys
1935                    400                 405                 410
1936  Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys
1937                    415                 420                 425
1938  Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His
1939                    430                 435                 440
1940  Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly
1941                    445                 450                 455
1942  Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu
1943                    460                 465                 470
1944  Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe
1945                    475                 480                 485
1946  Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro
1947                    490                 495                 500
1948  Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala
1949                    505                 510                 515
1950  Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp
1951                    520                 525                 530
1952  Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys
1953                    535                 540                 545
1954  Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro
1955                    550                 555                 560
1956  Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln
1957                    565                 570                 575
1958  Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro
1959                    580                 585                 590
1960  Leu Thr Leu Pro Ala Trp Leu His Ser Pro Xaa Arg Leu Pro Leu
1961                    595                 600                 605
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400 395 405 400 410 405 renumbering

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1962  Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly
1963                  610                 615                 620
1964  Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp
1965                  625                 630                 635
1966  Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly
1967                  640                 645                 650
1968  Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser Ala Leu Thr Leu
1969                  655                 660                 665
1970  Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr Xaa Ala Cys
1971                  670                 675                 680
1972  Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa Leu Ser
1973                  685                 690                 695
1974  Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly
1975                  700                 705                 710
1976  Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
1977                  715                 720                 725
1978  Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala
1979                  730                 735                 740
1980  Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val
1981                  745                 750                 755
1982  Gly Pro Xaa
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1984
1985
1986  -143-
1987
1988  SUBSTITUTE SHEET
1989
1990
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/367,013*

DATE: 05/05/2000
TIME: 11:03:42

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Line	Error	Original Text
33	Unknown or Misplaced Identifier	(B) (B) FILING DATE:
860	Entered (227) and Calc. Seq. Length (228) differ	(A) LENGTH: 227 amino acids
930	Entered (87) and Calc. Seq. Length (102) differ	(A) LENGTH: 87 amino acids
962	Entered (520) and Calc. Seq. Length (0) differ	(A) LENGTH: 520 nucleic acids
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972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
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Line	Error	Original Text
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
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979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
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1046	Entered (125) and Calc. Seq. Length (140) differ	(A) LENGTH: 125 amino acids
1481	Entered (411) and Calc. Seq. Length (406) differ	(A) LENGTH: 411 amino acids
1596	Entered (86) and Calc. Seq. Length (87) differ	(A) LENGTH: 86 amino acids
1682	Entered (566) and Calc. Seq. Length (562) differ	(A) LENGTH: 566 amino acids
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1872	Entered (757) and Calc. Seq. Length (753) differ	(A) LENGTH: 757 amino acids
1988	Wrong Amino Acid Designator	SUBSTITUTE SHEET
1988	Wrong Amino Acid Designator	SUBSTITUTE SHEET